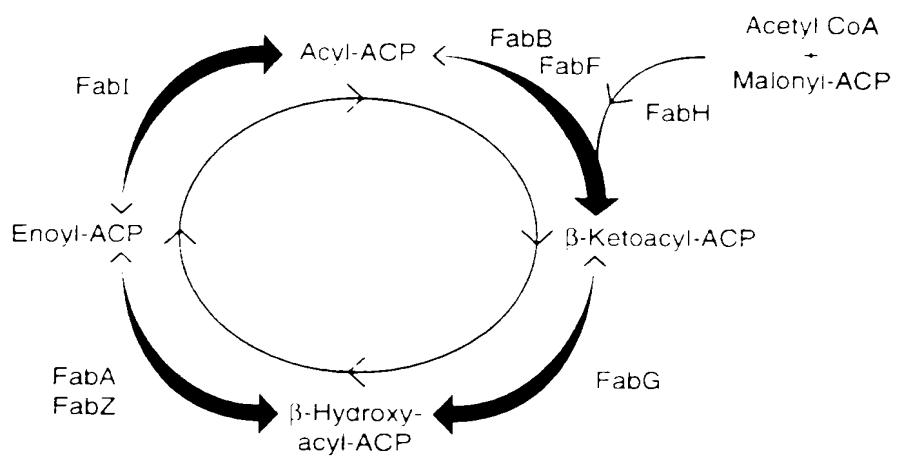


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Figure 1. The Cycle of Fatty Acid Elongation in Bacteria



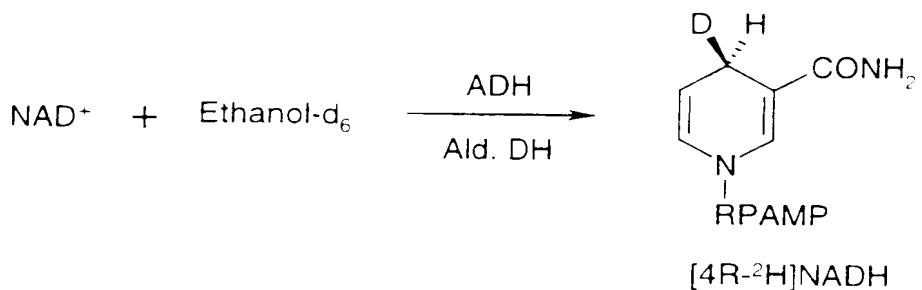
8/10/92 19

WO 00/70017

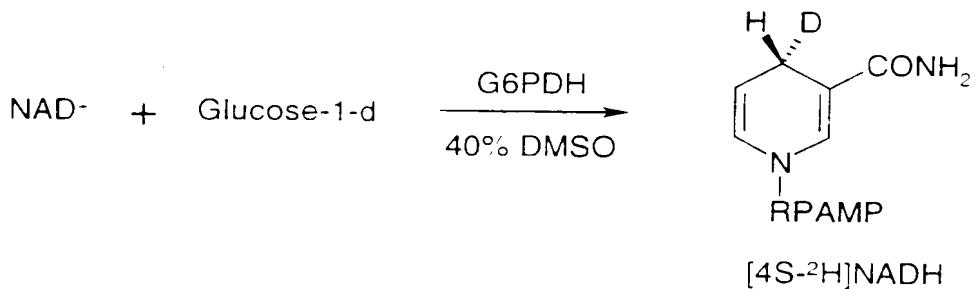
PCT/US00/12104

Figure 2. Synthesis of Deuterated Pyridine Nucleotides

## Synthesis of R-NADD



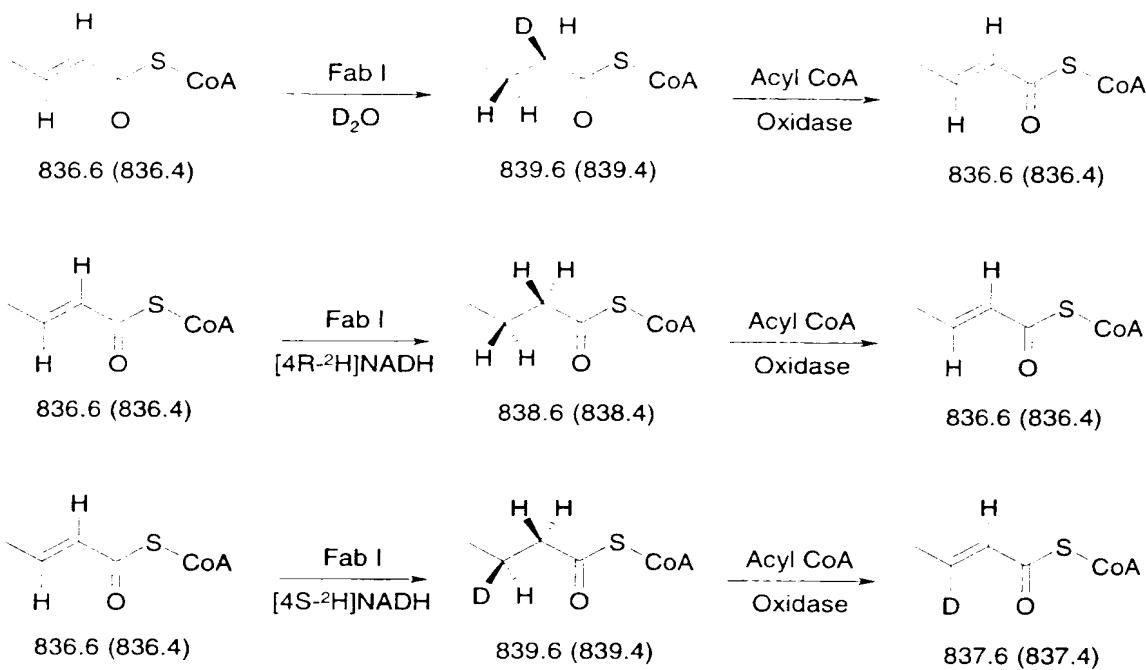
## Synthesis of S-NADD



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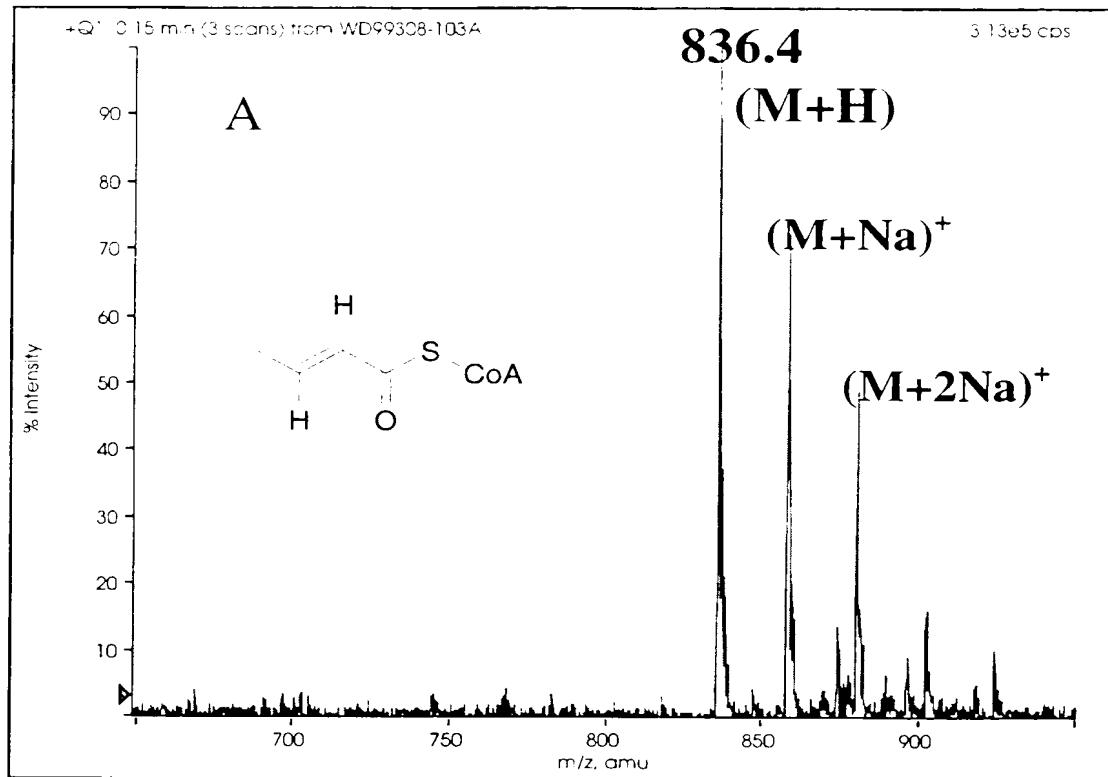
Figure 3. Predicted (Observed) Product Structures and  $(M+H)^+$ 's(Based on *E. coli* Fab I)

## Reaction



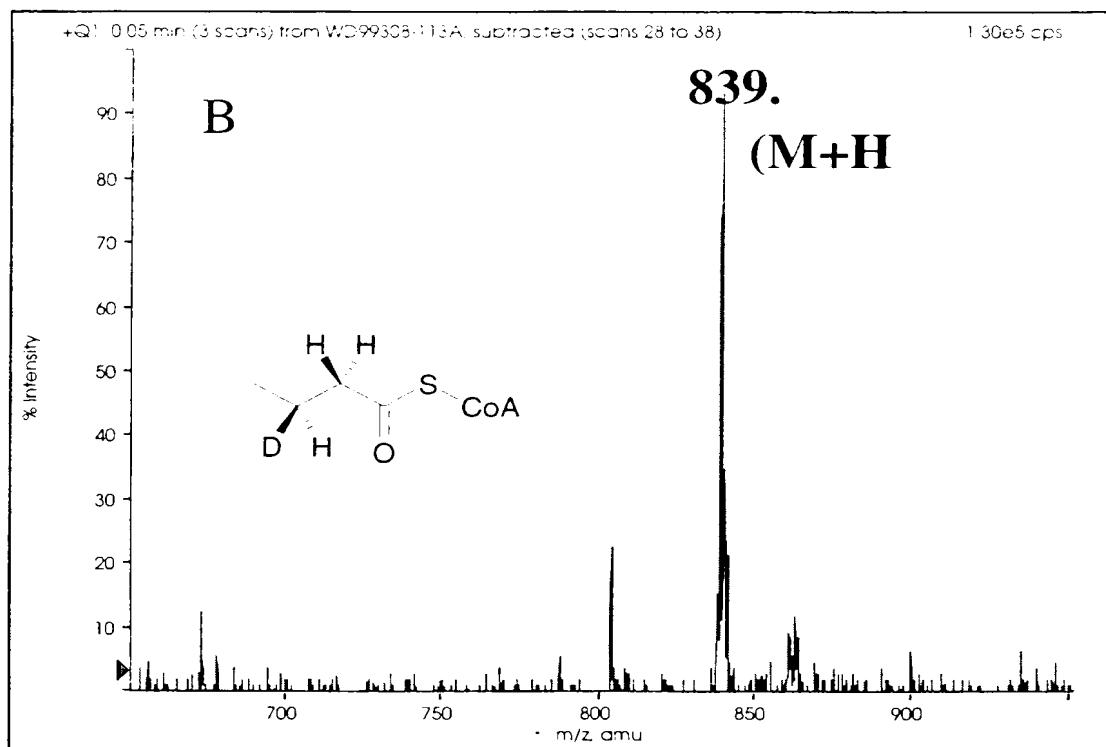
10/009319

Figure 4. Mass Spectra of Components from Reaction 3



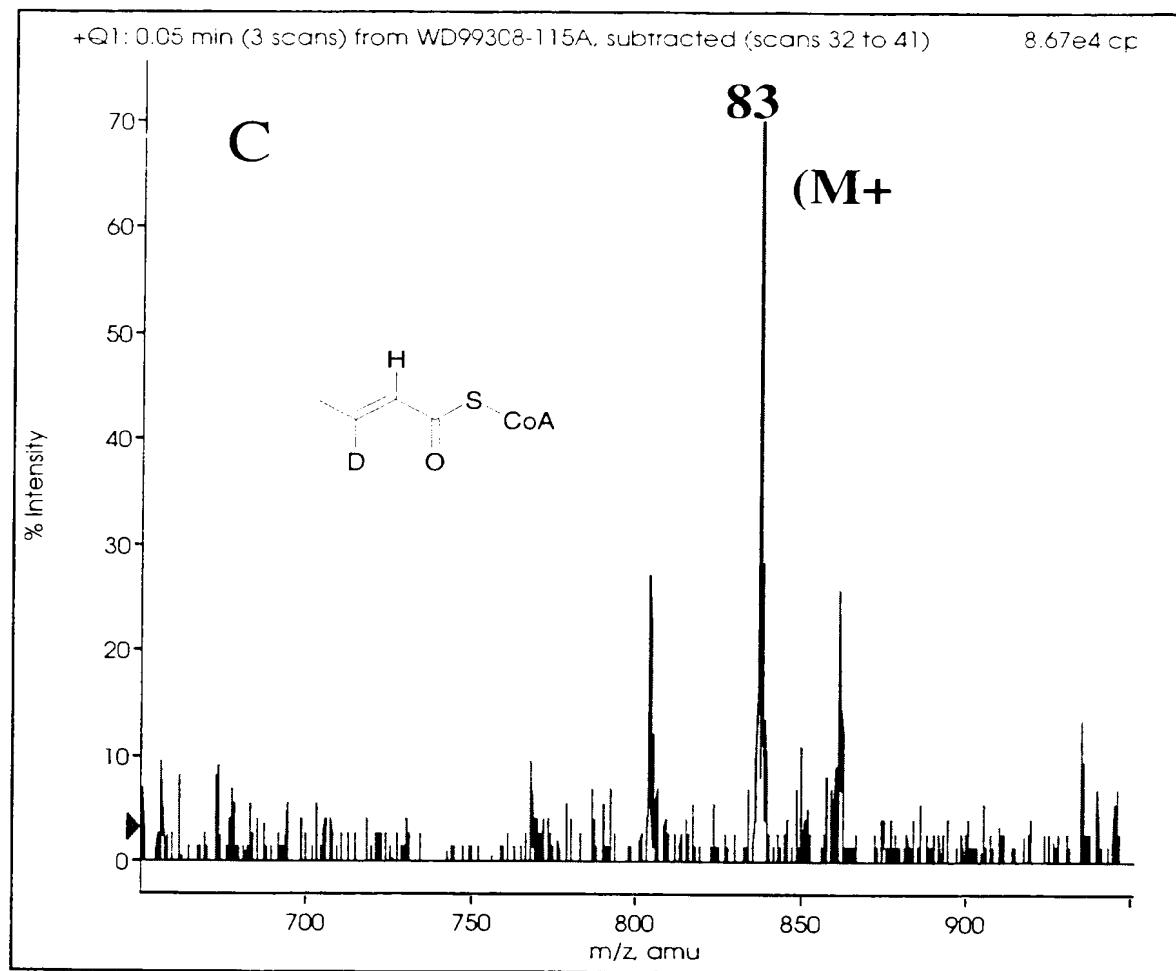
61029219

Figure 4 B

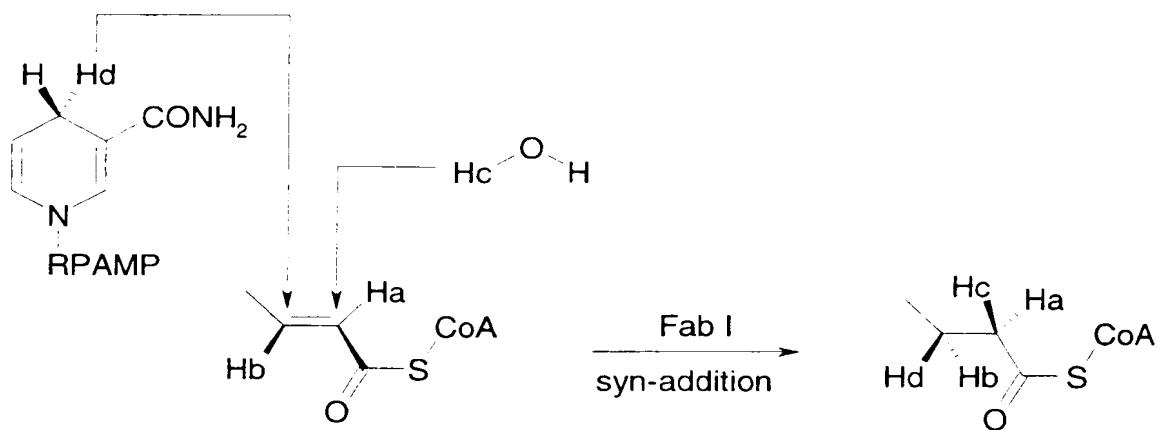


101029219

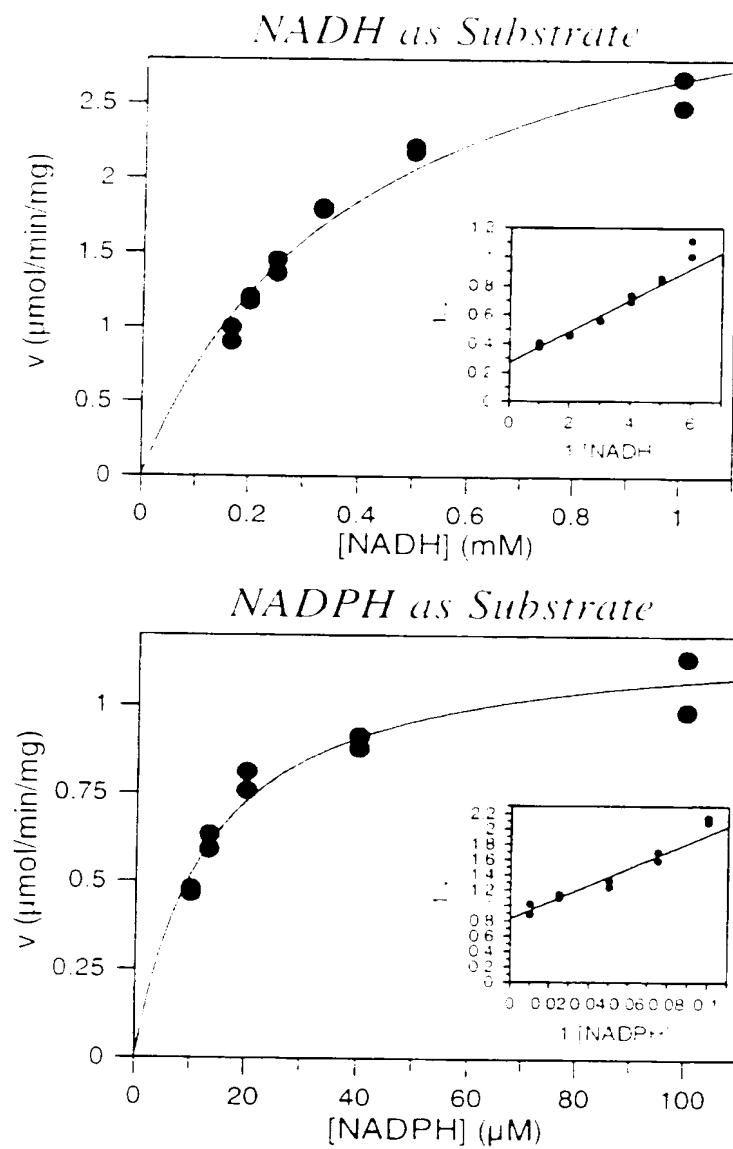
Figure 4 C



101079219

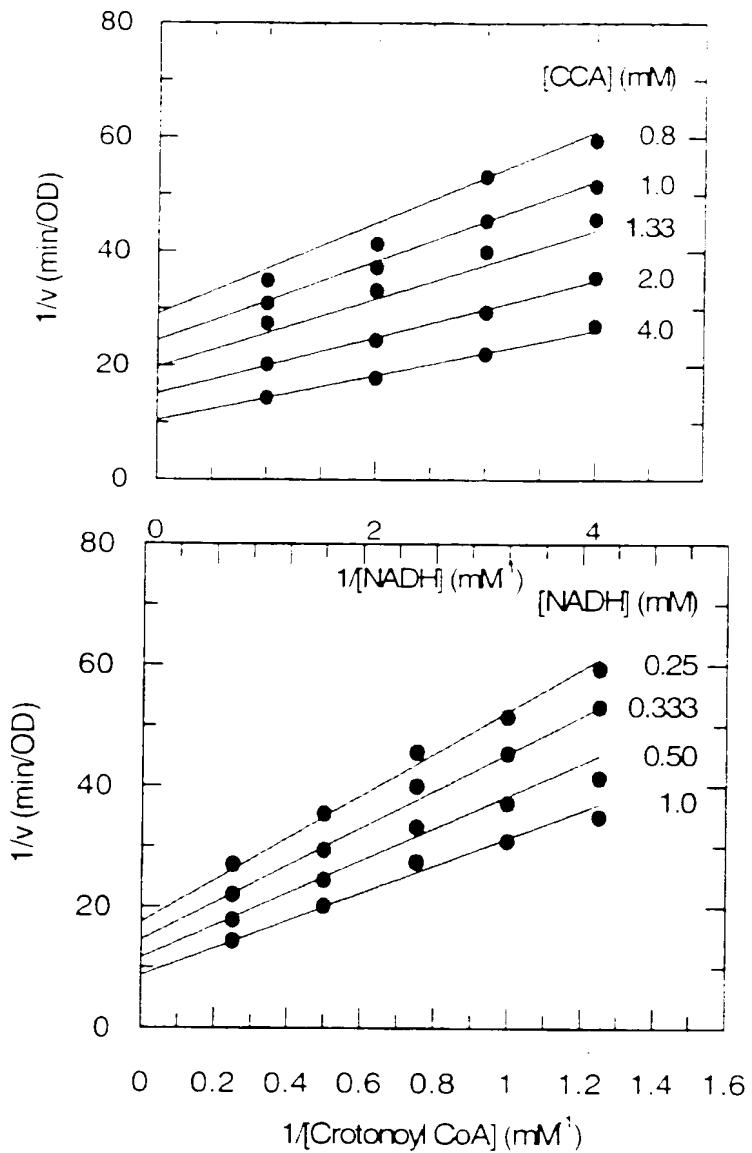
Figure 5. Stereochemical Course of *S. aureus* Fab I

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Figure 6. *S. aureus* Fab I Uses Both NADPH and NADH as Substrates

|  | NADH            | NADPH             |
|--|-----------------|-------------------|
| $V_m$ (app) ( $\mu\text{mol}/\text{min}/\text{mg}$ ) | 3.75 $\pm$ 0.23 | 1.21 $\pm$ 0.06   |
| $K_m$ (app) (mM)                                     | 0.41 $\pm$ 0.06 | 0.013 $\pm$ 0.002 |
| $K_m$ (app) CCA (mM)                                 | 3.5 $\pm$ 0.2   | 1.4 $\pm$ 0.4     |

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Figure 7. *S. aureus* Fab I Exhibits a Sequential Mechanism

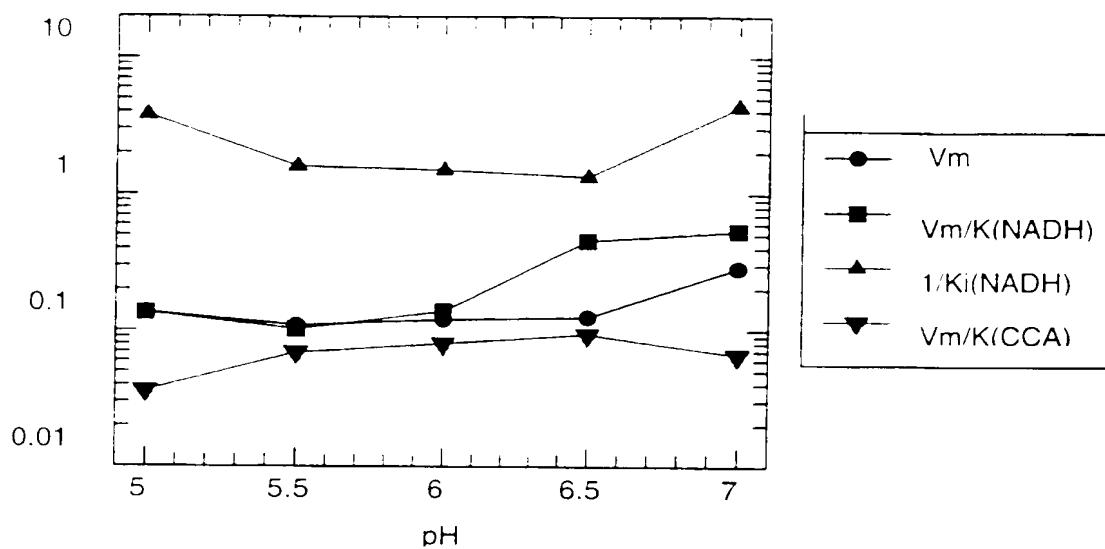
$$V_m = 0.18 \pm 0.02$$

$$K_a = 0.52 \pm 0.12 \text{ mM}$$

$$K_b = 3.3 \pm 0.6 \text{ mM}$$

$$K_{ia} = 0.22 \pm 0.06 \text{ mM}$$

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Figure 8. pH Profile of *S. aureus* Fab I

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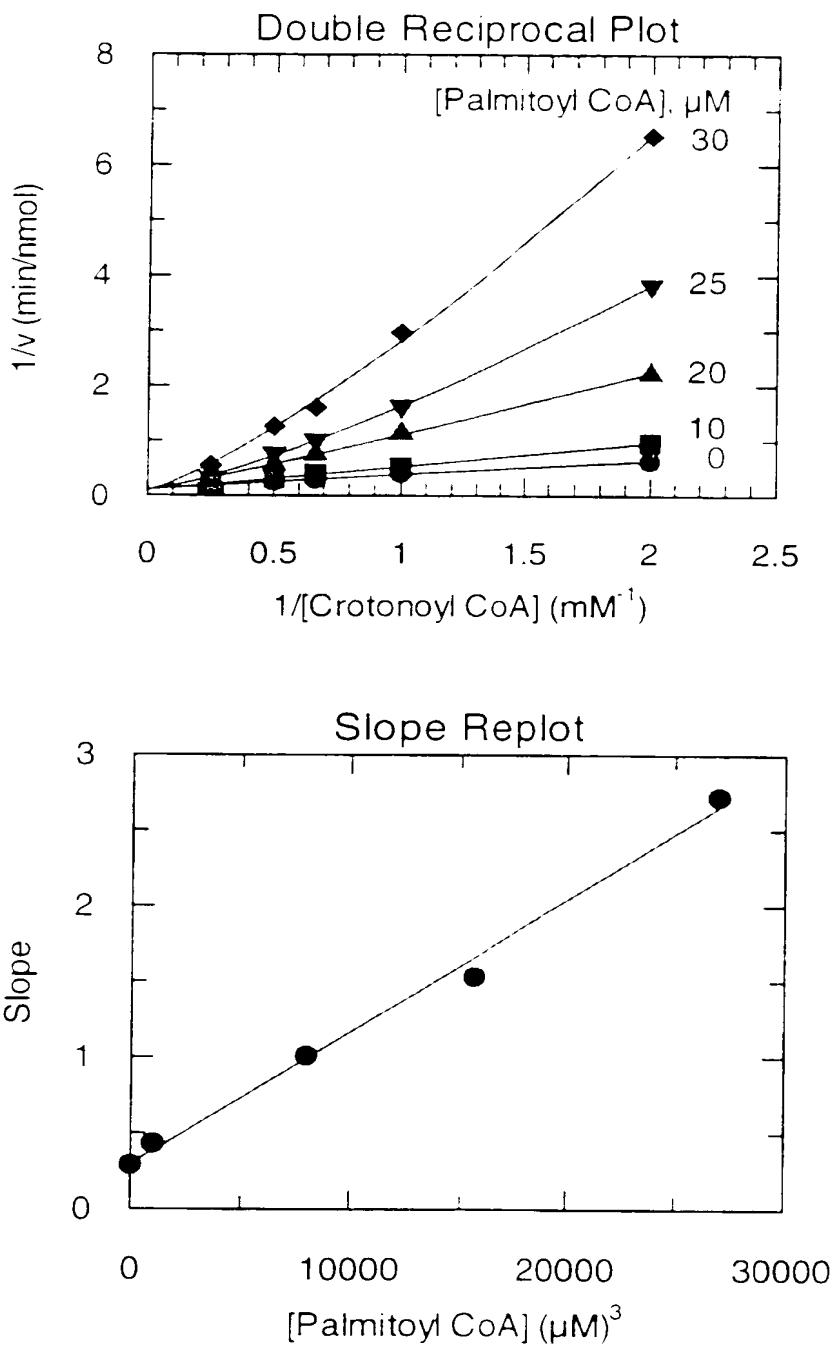
PCT/US00/12104

Figure 8 A Table 1. Inhibition by Saturated Fatty Acyl CoA's

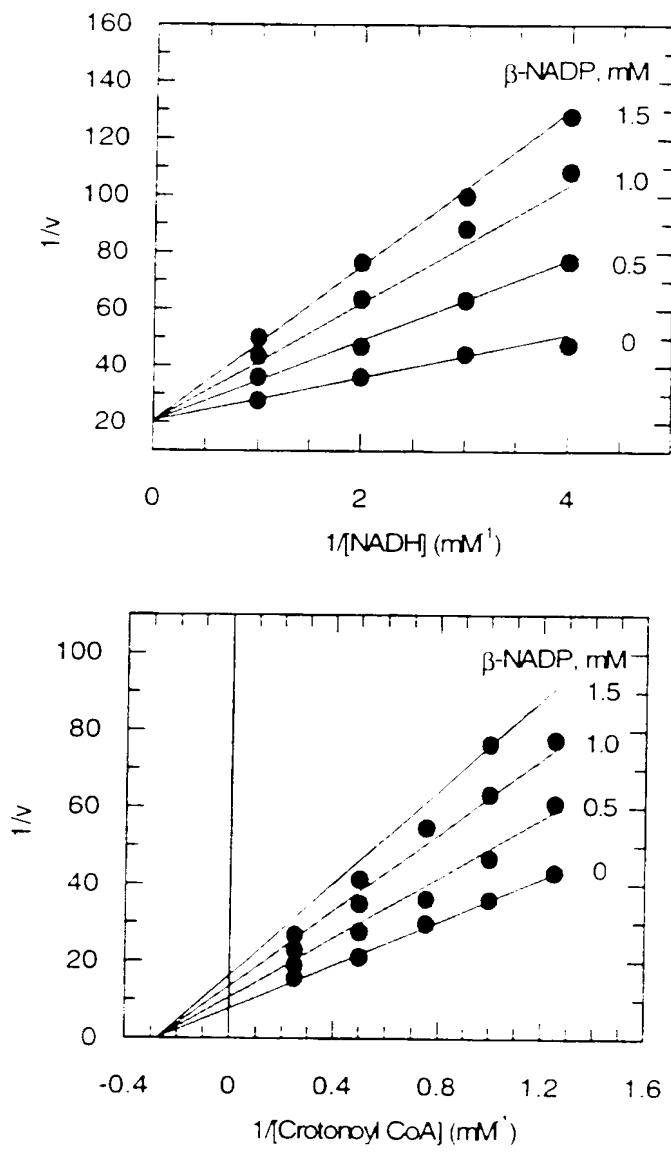
| <i>CoA Derivative</i> | <i>Mean IC<sub>50</sub> (μM) (n=2)</i> |
|-----------------------|--|
| <i>Acetyl</i>         | >>1000                                 |
| <i>n-Butyryl</i>      | >>1000                                 |
| <i>n-Hexanoyl</i>     | 576                                    |
| <i>n-Octanoyl</i>     | 248                                    |
| <i>n-Decanoyl</i>     | 226                                    |
| <i>Lauroyl</i>        | 48.4                                   |
| <i>Myristoyl</i>      | 23.1                                   |
| <i>Palmitoyl</i>      | 10.7                                   |

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Figure 9. Inhibition by Palmitoyl CoA



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Figure 10. Inhibition by  $\beta$ -NADP $+$ 

$$K_i = 0.58 \pm 0.03 \text{ mM}$$

Figure 11. Kinetic Model for Inhibition by  $\beta$ -NAPD<sup>+</sup>

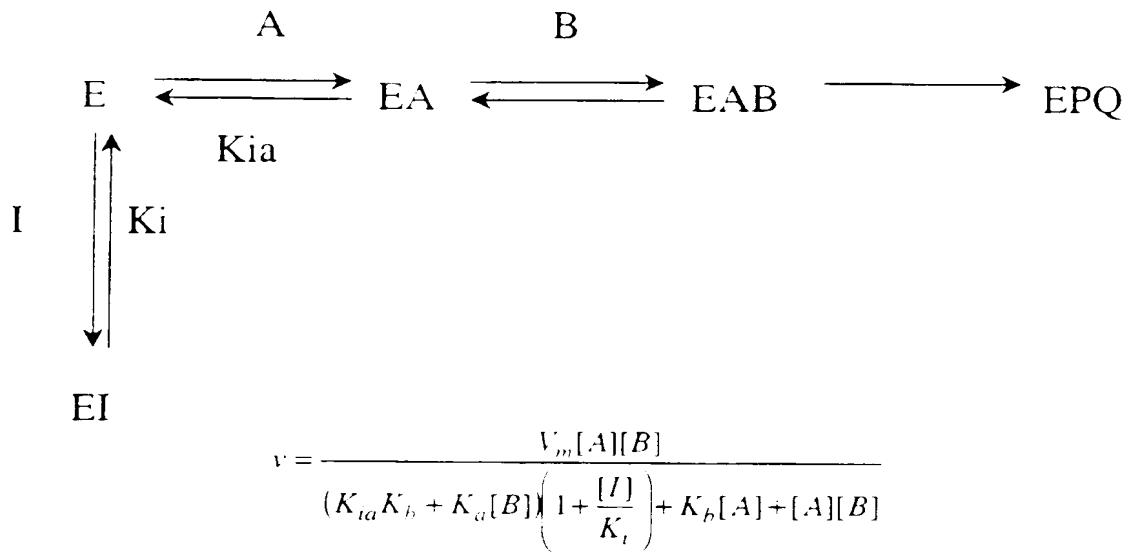
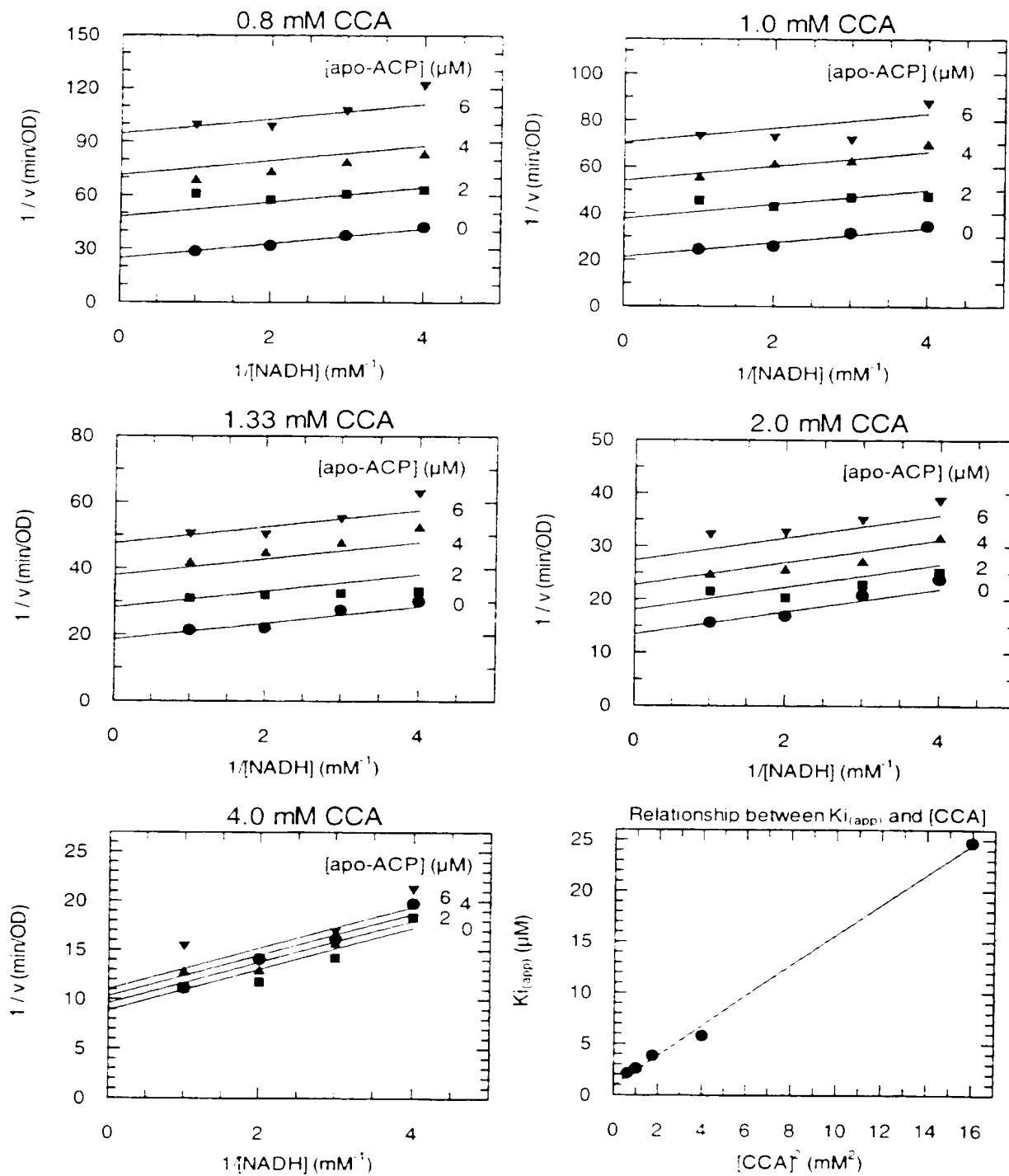


Figure 12. Inhibition by apo-ACP vs. NADH



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Figure 13. Inhibition by apo-ACP vs. CCA

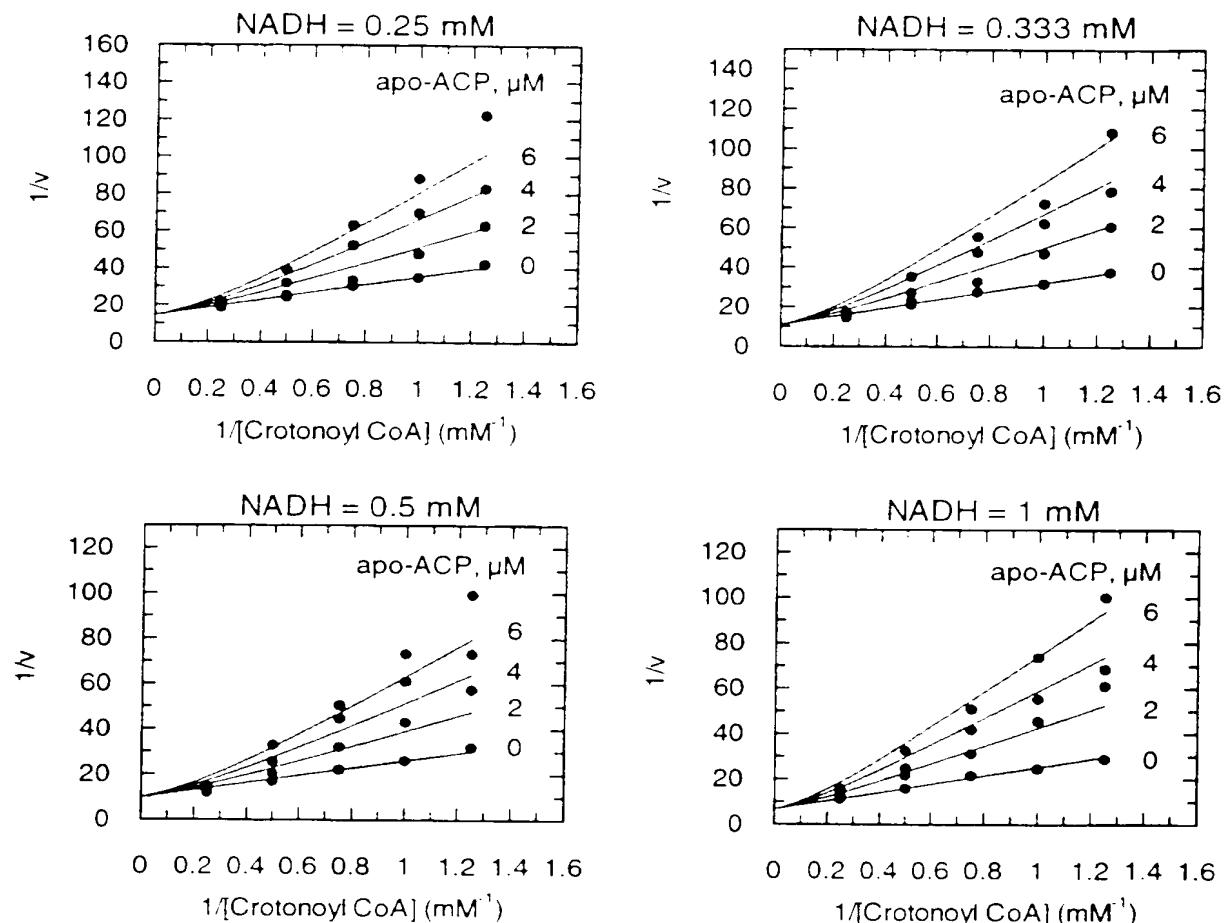
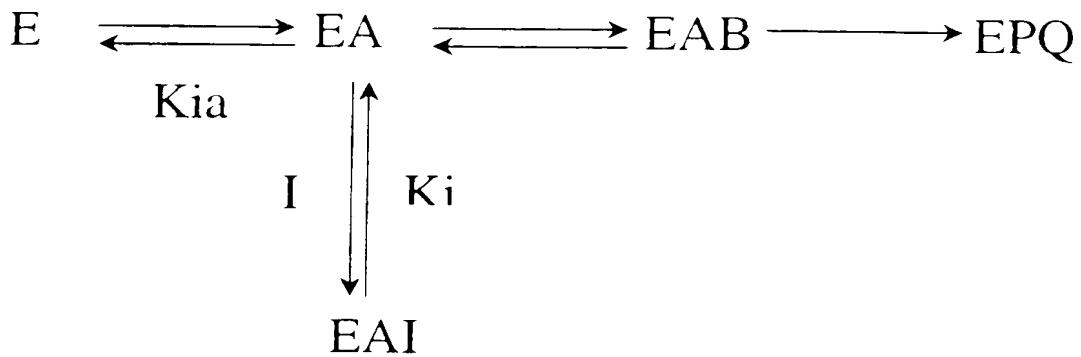


Figure 14. Minimal Kinetic Mechanism for Inhibition by apo-ACP



$$v = \frac{V_m[A][B]}{K_{ia}K_b + K_b[A] \left( 1 + \frac{[I]}{K_i} \right) + K_a[B] + [A][B]}$$

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Figure 15. Induced Cooperative Inhibition by apo-ACP

- Apo-ACP is uncompetitive versus NADH ( $K_i(\text{app})$ ) and is proportional to the square of [CCA]).
- Apo-ACP is competitive versus crotonoyl CoA and induces negative cooperativity with respect to Cca binding.

$$v = \frac{V_m \left[ \frac{[S]}{K_S} + \frac{[S]^2}{K_S^2} + \frac{[S][I]}{\alpha K_S K_I} \right]}{\left[ 1 + \frac{2[S]}{K_S} + \frac{[S]^2}{K_S^2} + \frac{2[I]}{K_I} + \frac{[I]^2}{K_I^2} + \frac{2[S][I]}{\alpha K_S K_I} \right]}$$

$$K_i = 3 \mu M$$

$$\alpha = 15$$

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## FIGURE 16

(SEQ ID NO:2)

1 MNLENKTTIV IMGIANKRSI AFGWAKVLDQ LGAKLWFTYR KERSRKELEK  
51 LLEQLNQPEA HLYQIDVQSD EEWINGFEDI GKDVGNIIDGV YHSIAFANME  
101 DLRGRFSETS REGFLLAQDI GSYSLTIVAH EAKKLMPEGG SIVATTYLGG  
151 EFAVQNYNRM GVAKASLEAN VKYLALDLGP DNIRVNAISA GPIRTLSAKG  
201 VGGFNTILKE IEERAPLKRN VDQVEVGKTA AVLLSDLSSG VTGENIHVDS  
251 GFHAIK

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## FIGURE 17

(SEQ ID NO:1)

1 ATGTTAAATC TTGAAAACAA AACATATGTC ATCATGGAA TCCCTAATAA  
51 GCGTAGTATT CCTTTGGTG TCGCTAAAGT TTTAGATCAA TTAGGTGCTA  
101 AATTAGTATT TACTTACCGT AAAGAACGTA GCCGTAAAGA GCTTGAAAAA  
151 TTATTAGAAC AATTAAATCA ACCAGAACGCC CACTTATATC AAATTGATGT  
201 TCAAAGCGAT GAAGAGGTTA TTAATGGTTT TGAGCAAATT GGTAAAGATG  
251 TTGGCAATAT TGATGGTGT A TATCATTCAA TCGCATTGCTA TAATATGGAA  
301 GACTTACGCG GACCGTTTTC TGAAACTTCA CGTGAAGCCT TCTTGTAGC  
351 TCAAGACATT AGTTCTTACT CATTAAACAAT TGTGGCTCAT GAAGCTAAAAA  
401 AATTAAATGCC AGAAGGTGGT AGCATGGTG CAACAAACATA TTTAGGTGGC  
451 GAATT CGCAG TTCAAAATTA TAATGTGATG GGTGTTGCTA AAGCGAGCTT  
501 AGAAGCAAAT GTAAATATT TAGCATTAGA CTTAGGTCT GATAATATTC  
551 GCGTTAATGC AATTCAGCT GGTCCAATCC GTACATTAAG TGCAAAAGGT  
601 GTGGGTGGTT TCAATACAAT TCTTAAAGAA ATCGAAGAGC GTGCACCTTT  
651 AAAACGTAAC GTTGATCAAG TAGAAGTAGG TAAAACAGCG GCTTACTTRT  
701 TAAGTGACTT ATCAAGTGGC GTTACAGGTG AAAATATTCA TGTAGATAGC  
751 GGATTCCACG CAATTAAATA A